

(1) GENERAL INFORMATION:

(i) APPLICANT: GOTO, Masaaki
TSUDA, Eisuke
MOCHIZUKI, Shin'ichi
YANO, Kazuki
KOBAYASHI, Fumie
SHIMA, Nobuyuki
YASUDA, Hisataka
NAKAGAWA, Nobuaki
MORINAGA, Tomonori
UEDA, Masatsugu
HIGASHIO, Kanji

(ii) TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins

(iii) NUMBER OF SEQUENCES: 108

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Testa, Hurwitz & Thibault
(B) STREET: 125 High St.
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0 Version #1.30

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(B) FILING DATE:
(C) CLASSIFICATION:

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(B) FILING DATE: 20-FEB-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CAMPBELL, Paula A.
(B) REGISTRATION NUMBER: 32,503
(C) REFERENCE/DOCKET NUMBER: FJN-060

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 248-7000
(B) TELEFAX: (617) 248-7100

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..6
(D) OTHER INFORMATION: /note= "(an internal amino acid
sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Tyr His Phe Pro Lys
1 5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..14
(D) OTHER INFORMATION: /note= "(an internal amino acid
sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Gln His Ser Xaa Gln Glu Gln Thr Phe Gln Leu Xaa Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..12
(D) OTHER INFORMATION: /note= "(an internal amino acid
sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

[illegible]

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(ix) FEATURE:
  (A) NAME/KEY: Protein
  (B) LOCATION: 1..380
  (D) OTHER INFORMATION: /note= "(OCIF protein without
signal peptide)"

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Glu 1	Thr	Phe	Pro 5	Pro 5	Lys	Tyr	Leu	His 10	Tyr 10	Asp	Glu	Glu	Thr	Ser 15	His
Gln	Leu	Leu	Cys 20	Asp	Lys	Cys	Pro 25	Pro 25	Gly	Thr	Tyr	Leu	Lys 30	Gln	His
Cys	Thr	Ala 35	Lys	Trp	Lys	Thr 40	Val 40	Cys	Ala	Pro	Cys 45	Pro 45	Asp	His	Tyr
Tyr	Thr 50	Asp	Ser	Trp	His 55	Thr 55	Ser	Asp	Glu	Cys 60	Leu 60	Tyr	Cys	Ser	Pro
Val 65	Cys	Lys	Glu	Leu	Gln 70	Tyr 70	Val	Lys	Gln 75	Glu 75	Cys	Asn	Arg	Thr 80	His 80
Asn	Arg	Val	Cys 85	Glu 85	Cys	Lys	Glu	Gly 90	Arg 90	Tyr	Leu	Glu	Ile 95	Glu 95	Phe
Cys	Leu	Lys 100	His 100	Arg	Ser	Cys	Pro 105	Pro 105	Gly	Phe	Gly	Val 110	Val 110	Gln	Ala
Gly	Thr 115	Pro 115	Glu	Arg	Asn	Thr 120	Val 120	Cys	Lys	Arg	Cys 125	Pro 125	Asp	Gly	Phe
Phe 130	Ser 130	Asn	Glu	Thr	Ser 135	Ser 135	Lys	Ala	Pro	Cys 140	Arg 140	Lys	His	Thr	Asn
Cys 145	Ser	Val	Phe	Gly 150	Leu 150	Leu	Leu	Thr	Gln 155	Lys 155	Gly	Asn	Ala	Thr 160	His 160
Asp	Asn	Ile	Cys 165	Ser 165	Gly	Asn	Ser	Glu 170	Ser 170	Thr	Gln	Lys	Cys 175	Gly 175	Ile
Asp	Val	Thr 180	Leu 180	Cys	Glu	Glu	Ala 185	Phe 185	Phe	Arg	Phe	Ala 190	Val 190	Pro	Thr
Lys	Phe 195	Thr 195	Pro	Asn	Trp	Leu 200	Ser 200	Val	Leu	Val	Asp 205	Asn 205	Leu	Pro	Gly
Thr 210	Lys 210	Val	Asn	Ala	Glu 215	Ser 215	Val	Glu	Arg	Ile 220	Lys 220	Arg	Gln	His	Ser
Ser 225	Gln	Glu	Gln	Thr 230	Phe 230	Gln	Leu	Leu	Lys 235	Leu 235	Trp	Lys	His	Gln 240	Asn 240
Lys	Asp	Gln	Asp 245	Ile 245	Val	Lys	Lys	Ile 250	Ile 250	Gln	Asp	Ile	Asp 255	Leu 255	Cys
Glu	Asn	Ser 260	Val 260	Gln	Arg	His	Ile 265	Gly 265	His	Ala	Asn	Leu	Thr 270	Phe	Glu
Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala

Gly Val Val Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 110 115 120
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
 125 130 135
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
 140 145 150 155
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
 160 165 170
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 175 180 185
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
 190 195 200
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 205 210 215
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 220 225 230 235
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
 240 245 250
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
 255 260 265
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
 270 275 280
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
 285 290 295
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 300 305 310 315
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
 320 325 330
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
 335 340 345
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
 350 355 360
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
 365 370 375
 Leu
 380

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1206

ATGAACAACACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAAG	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCTTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTTCTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTCAAAGA	CGTACCACTT	TCCCAAACT	1080
GTCACTCAGA	GTCTAAAGAA	GACCATCAGG	TTCTTCACA	GCTTCACAAT	GTACAAATTG	1140
TATCAGAAGT	TATTTTTAGA	AATGATAGGT	AACCAGGTCC	AATCAGTAAA	AATAAGCTGC	1200
TTATAA						1206

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) **FEATURE:**

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

6

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1185
- (D) OTHER INFORMATION: /note= "(OCIF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
CTATACTGCA GCCCCGTGTG CAAGGAGTGC AATCGCACCC ACAACCGCGT GTGCGAATGC 300
AAGGAAGGGC GCTACCTTGA GATAGAGTTC TGCTTGAAAC ATAGGAGCTG CCCTCCTGGA 360
TTTGAGTGG TGCAAGCTGG AACCCAGAG CGAAATACAG TTGCAAAAG ATGTCCAGAT 420
GGGTTCTTCT CAAATGAGAC GTCATCTAAA GCACCCTGTA GAAAACACAC AAATTGCAGT 480
GTCTTTGGTC TCCTGCTAAC TCAGAAAGGA AATGCAACAC ACGACAACAT ATGTTCCGGA 540
AACAGTGAAT CAACTCAAAA ATGTGGAATA GATGTTACCC TGTGTGAGGA GGCATTCTTC 600
AGGTTTGTG TTCCTACAAA GTTTACGCCT AACTGGCTTA GTGTCTTGGT AGACAATTTG 660
CCTGGCACCA AAGTAAACGC AGAGAGTGTG GAGAGGATAA AACGGCAACA CAGCTCACAA 720
GAACAGACTT TCCAGCTGCT GAAGTTATGG AAACATCAAA ACAAAGACCA AGATATAGTC 780
AAGAAGATCA TCCAAGATAT TGACCTCTGT GAAAACAGCG TGCAGCGGCA CATTGGACAT 840
GCTAACCTCA CCTTCGAGCA GCTTCGTAGC TTGATGGAAA GCTTACCGGG AAAGAAAGTG 900
GGAGCAGAAG ACATTGAAAA AACAATAAAG GCATGCAAAC CAGTGACCA GATCCTGAAG 960
CTGCTCAGTT TGTGGCGAAT AAAAAATGGC GACCAAGACA CCTTGAAGGG CCTAATGCAC 1020
GCACTAAAGC ACTCAAAGAC GTACCACTTT CCCAAACTG TCACTCAGAG TCTAAAGAAG 1080
ACCATCAGGT TCCTTCACAG CTTCACAATG TACAAATTGT ATCAGAAGTT ATTTTGTAGAA 1140
ATGATAGGTA ACCAGGTCCA ATCAGTAAAA ATAAGCTGCT TATAA 1185

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Figure 1. The 12 cases of the 1997-1998 season. The cases are arranged in order of their first onset date. The cases are numbered 1 through 12. The cases are arranged in order of their first onset date. The cases are numbered 1 through 12.

(A) NAME/KEY: Protein

(D) OTHER INFORMATION: /note= "(OCIF2)"

(A) NAME/KEY: Peptide

(B) LOCATION: -21..0

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Cys Asn Arg Thr His Asn Arg
60 65 70 75

Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu
80 85 90

Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
95 100 105

Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser
110 115 120

Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser
125 130 135

Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn
140 145 150 155

Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val
160 165 170

Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe
175 180 185

Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys
190 195 200

Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	Ser	Gln
	205					210					215				

Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp
220 225 230 235

Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn
240 245 250

Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu

9

Case	Age	Sex	Duration	Location	Findings	Comments
1	25	M	10 years	Left eye	Normal	
2	30	F	5 years	Right eye	Normal	
3	35	M	15 years	Left eye	Normal	
4	40	F	20 years	Right eye	Normal	
5	45	M	25 years	Left eye	Normal	
6	50	F	30 years	Right eye	Normal	
7	55	M	35 years	Left eye	Normal	
8	60	F	40 years	Right eye	Normal	
9	65	M	45 years	Left eye	Normal	
10	70	F	50 years	Right eye	Normal	
11	75	M	55 years	Left eye	Normal	
12	80	F	60 years	Right eye	Normal	
13	85	M	65 years	Left eye	Normal	
14	90	F	70 years	Right eye	Normal	
15	95	M	75 years	Left eye	Normal	

AACAAAGACC AA TAC-1 CAAGAAGATC ATCCAAGATA TTGAC TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC AGTTTGTGGC GAATAAAAAA TGGCGACCAA 900
 GACACCTTGA AGGGCCTAAT GCACGCACTA AAGCACTCAA AGACGTACCA CTTTCCCAAA 960
 ACTGTCACTC AGAGTCTAAA GAAGACCATC AGGTTCTTTC ACAGCTTCAC AATGTACAAA 1020
 TTGTATCAGA AGTTATTTTT AGAAATGATA GGTAACCAGG TCCAATCAGT AAAAATAAGC 1080
 TGCTTATAA 1089

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..341
 (D) OTHER INFORMATION: /note= "(OCIF3)"

- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 5 10
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 30 35 40
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 45 50 55
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
 60 65 70 75
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
 80 85 90
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
 95 100 105
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 110 115 120
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
 125 130 135
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
 140 145 150 155

	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440</
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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 465 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

11

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..133
 - (D) OTHER INFORMATION: /note= "(OCIF4)"

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Met Asn Lys Leu Leu Cys Cys Ser Leu Val Phe Leu Asp Ile Ser Ile
-20                      -15                      -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5                      1                      5                      10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15                      20                      25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
30                      35                      40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45                      50                      55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
60                      65                      70                      75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
80                      85                      90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
95                      100                      105

Gly Val Val Gln Ala Gly Thr Cys Gln Cys Ala Ala Lys Leu Ile Arg
110                      115                      120

Ile Met Gln Ser Gln Ile Val Val Thr Val
125                      130

```

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

[illegible]

ATGAACAAGT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GATGCAGGAG	AAGACCCAAG	420
CCACAGATAT	GTATCTGA					438

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(ix) FEATURE:

```
(A) NAME/KEY: Peptide
(B) LOCATION: -21..0
```

Met	Asn	Lys	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
-20						-15					-10					
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5				1				5						10		
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20					25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
	30						35					40				
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
45						50					55					
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60					65					70					75	
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
				80					85					90		
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	

Gly Val Val Gln Ala Gly Cys Arg Arg Arg Pro Lys Pro Gln Ile Cys
 110 115 120

Ile

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer T3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATTAACCCT CACTAAAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..22
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer T7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAATACGAC TCACTATAGG GC

22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACATCAAAAC AAAGACCAAG

20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCTTGGTCTT TGTTTTGATG

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTATTCGCCA CAACTGAGC

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTGTGAAGCT GTGAAGGAAC

20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF5)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCTCAGTTTG TGGCGAATAA

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF6)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGGGAGCAG AAGACATTGA

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AATGAACAAC TTGCTGTGCT

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF8)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGACAAATGT CCTCCTGGTA

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF9)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGGTAGGTAC CAGGAGGACA

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF10)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGCTGCCCT CCTGGATTG

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF11)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAAACTGTAT TTCGCTCTGG

20

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "synthetic DNA (primer

IF12) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGTGAGGAG GCATTCTTCA

20

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..32
(D) OTHER INFORMATION: /note= "synthetic DNA (primer

C19SF) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATCAACTC AAAAAAGTGG AATAGATGTT AC

32

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..32
(D) OTHER INFORMATION: /note= "synthetic DNA (primer

C19SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTAACATCTA TTCCAATTTT TTGAGTTGAT TC

32

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Case	Age	Sex	Duration	Location	Findings	Comments
1	45	M	10 years	Right eye	Small, well-circumscribed, pigmented lesion	Benign melanocytic nevus
2	60	F	5 years	Left eye	Large, irregular, pigmented lesion	Malignant melanoma
3	30	M	2 years	Right eye	Small, well-circumscribed, pigmented lesion	Benign melanocytic nevus
4	55	F	8 years	Left eye	Large, irregular, pigmented lesion	Malignant melanoma
5	40	M	3 years	Right eye	Small, well-circumscribed, pigmented lesion	Benign melanocytic nevus
6	65	F	12 years	Left eye	Large, irregular, pigmented lesion	Malignant melanoma
7	35	M	1 year	Right eye	Small, well-circumscribed, pigmented lesion	Benign melanocytic nevus
8	50	F	6 years	Left eye	Large, irregular, pigmented lesion	Malignant melanoma
9	42	M	4 years	Right eye	Small, well-circumscribed, pigmented lesion	Benign melanocytic nevus
10	58	F	7 years	Left eye	Large, irregular, pigmented lesion	Malignant melanoma

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

31

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCAGTAAAAA TAAGCAGCTT ATAAGTGGCC A

31

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer C23SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TGGCCAGTTA TAAGCTGCTT ATTTTACTG A

31

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF14) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTGGGGTTTA TTGGAGGAGA TG

22

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR1F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCACCCAGG AACCTTGCCC TGACCACTAC TACACA

36

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR1R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTCAGGGCAA GGTTCCTGGG TGGTCCACTT AATGGA

36

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR2F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACCGTGTGCG CCGAATGCAA GGAAGGGCGC TACCTT

36

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR2R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTCCTTGCAT TCGGCGCACA CGGTCTTCCA CTTTGC

36

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR3F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AACCGCGTGT GCAGATGTCC AGATGGGTTC TTCTCA

36

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR3R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTGGACAT CTGCACACGC GGTGTGGGT GCGATT

36

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR4F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAGTTTGCA AATCCGAAA CAGTGAATCA ACTCAA

36

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR4R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTGTTTCCG GATTGCAAA CTGTATTTTCG CTCTGG

36

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DDD1F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AATGTGGAAT AGATATTGAC CTCTGTGAAA ACAGCG

36

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DDD1R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGAGGTCAAT ATCTATTCCA CATTTTGTGAG TTGATT

36

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DDD2F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGATCATCCA AGACGCACTA AAGCACTCAA AGACGT

36

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DDD2R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGTTTAGTGC GTCTTGGATG ATCTTCTTGA CTATAT

36

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer XhoI F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCTCGAGCG CCCAGCCGCC GCCTCCAAG

29

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF16) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTTGAGTGCT TTAGTGCCTG

20

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CL

F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TCAGTAAAAA TAAGCTAACT GGAAATGGCC

30

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CL

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCCATTTCC AGTTAGCTTA TTTTACTGA

30

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..29
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CC

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCGGATCCTC AGTGCTTTAG TCGTGTCAT

29

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCD2

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCGGATCCTC ATTGGATGAT CTTCTTGAC

29

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCD1

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCGGATCCTC ATATTCCACA TTTTGTAGT

29

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCR4

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCGGATCCTC ATTTGCAAAC TGTATTTTCG

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

CCGGATCCTC ATTCGCACAC GCGGTTGTG

29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```
(ix) FEATURE:
      (A) NAME/KEY: Peptide
      (B) LOCATION: -21..0
```

```
(ix) FEATURE:
      (A) NAME/KEY: Protein
      (B) LOCATION: 1..380
      (D) OTHER INFORMATION: /note= "OCIF-C19S"
```

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
-20						-15					-10				
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp
-5					1				5					10	
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr
			15					20					25		
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro
		30					35					40			
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys
	45					50						55			
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu
60					65					70					75
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr
				80					85					90	
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe
			95					100					105		
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg
		110					115					120			
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys
	125					130					135				
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys
140					145					150					155
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr

170

29

Figure 1 displays 12 histograms, labeled x_0 through x_{11} , showing the distribution of the number of non-zero elements in the vector x_k . The x-axis represents the number of non-zero elements (0 to 10), and the y-axis represents the count (0 to 10). The distributions are roughly bell-shaped and centered around 5, with the peak count increasing from 10 at x_0 to 12 at x_{11} .

Case	Age	Sex	Duration	Location	Findings	Diagnosis
1	25	M	10 years	Right eye	Small, dark, pigmented lesion	Choroidal melanoma
2	35	F	5 years	Left eye	Large, white, fibrous lesion	Choroidal melanoma
3	45	M	15 years	Right eye	Small, dark, pigmented lesion	Choroidal melanoma
4	55	F	20 years	Left eye	Large, white, fibrous lesion	Choroidal melanoma
5	65	M	25 years	Right eye	Small, dark, pigmented lesion	Choroidal melanoma
6	75	F	30 years	Left eye	Large, white, fibrous lesion	Choroidal melanoma
7	85	M	35 years	Right eye	Small, dark, pigmented lesion	Choroidal melanoma
8	95	F	40 years	Left eye	Large, white, fibrous lesion	Choroidal melanoma

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```
(ix) FEATURE:
      (A) NAME/KEY: Peptide
      (B) LOCATION: -21..0
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

31

Gln Lys Cys Ile Asp Val Thr Leu Cys Glu Glu Phe Phe Arg
 180 185
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
 190 195 200
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 205 210 215
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 220 225 230 235
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
 240 245 250
 Asp Ile Asp Leu Ser Glu Asn Ser Val Gln Arg His Ile Gly His Ala
 255 260 265
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
 270 275 280
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
 285 290 295
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 300 305 310 315
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
 320 325 330
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
 335 340 345
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
 350 355 360
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
 365 370 375
 Leu
 380

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "OCIF-C22S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10

Lys Trp Th Gln Glu Thr Phe Pro Pro Lys Leu His Tyr Asp
 -5 1 5 10
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 30 35 40
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 45 50 55
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
 60 65 70 75
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
 80 85 90
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
 95 100 105
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 110 115 120
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
 125 130 135
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
 140 145 150 155
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
 160 165 170
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 175 180 185
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
 190 195 200
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 205 210 215
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 220 225 230 235
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
 240 245 250
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
 255 260 265
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
 270 275 280
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Ser Lys
 285 290 295
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 300 305 310 315
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
 320 325 330
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
 335 340 345
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
 350 355 360

Phe Leu Gly Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
365 370 375

Leu
380

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

```
(ix) FEATURE:
      (A) NAME/KEY: Peptide
      (B) LOCATION: -21..0
```

```
(ix) FEATURE:
      (A) NAME/KEY: Protein
      (B) LOCATION: 1..380
      (D) OTHER INFORMATION: /note= "OCIF-C23S"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
-20						-15					-10				
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp
-5				1					5					10	
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr
			15					20					25		
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro
		30					35					40			
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys
	45					50					55				
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu
60					65					70					75
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr
				80					85					90	
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe
			95					100					105		
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg
		110					115					120			
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys
	125					130					135				
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys
140					145					150					155
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr
				160					165					170	
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg
			175					180					185		

Trp His 15 Ser Asp Glu Cys Leu Tyr Cys Ser 20 Val Cys Lys Glu 25
 Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys 30 35 40
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His 45 50 55
 Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu 60 65 70 75
 Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu 80 85 90
 Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe 95 100 105
 Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys 110 115 120
 Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu 125 130 135
 Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro 140 145 150 155
 Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn 160 165 170
 Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln 175 180 185
 Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp 190 195 200
 Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val 205 210 215
 Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser 220 225 230 235
 Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu 240 245 250
 Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu 255 260 265
 Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu 270 275 280
 Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val 285 290 295
 Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met 300 305 310 315
 Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val 320 325 330
 Gln Ser Val Lys Ile Ser Cys Leu 335

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 amino acids

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

```
(ix) FEATURE:
      (A) NAME/KEY: Peptide
      (B) LOCATION: -21..0
```

```
(ix) FEATURE:
      (A) NAME/KEY: Protein
      (B) LOCATION: 1..338
      (D) OTHER INFORMATION: /note= "OCIF-DCR2"
```

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
-20						-15					-10				
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp
-5				1					5					10	
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr
			15					20					25		
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Glu
		30					35					40			
Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg
	45					50					55				
Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg
60					65					70					75
Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr
				80					85					90	
Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly
			95					100					105		
Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser
		110					115					120			
Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys
	125					130					135				
Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn
140					145					150					155
Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala
				160					165					170	
Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr
			175					180					185		
Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile
		190					195					200			
Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln
	205					210					215				
Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu
220					225					230					235
Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys

38

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- ```
(A) NAME/KEY: Peptide
(B) LOCATION: -21..0
```

(A) NAME/KEY: Protein  
(B) LOCATION: 1..338  
(D) OTHER INFORMATION: /note= "OCIF-DCR4"

## Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile

-10

40

[illegible]



(ii) MOLECULE TYPE: protein

```
(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..305
 (D) OTHER INFORMATION: /note= "OCIF-DDD1"
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Asn | Leu | Leu | Cys | Cys | Ala | Leu | Val | Phe | Leu | Asp | Ile | Ser | Ile |
| -20 |     |     |     |     |     | -15 |     |     |     |     | -10 |     |     |     |     |
| Lys | Trp | Thr | Thr | Gln | Glu | Thr | Phe | Pro | Pro | Lys | Tyr | Leu | His | Tyr | Asp |
| -5  |     |     |     | 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |
| Glu | Glu | Thr | Ser | His | Gln | Leu | Leu | Cys | Asp | Lys | Cys | Pro | Pro | Gly | Thr |
|     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |
| Tyr | Leu | Lys | Gln | His | Cys | Thr | Ala | Lys | Trp | Lys | Thr | Val | Cys | Ala | Pro |
|     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |
| Cys | Pro | Asp | His | Tyr | Tyr | Thr | Asp | Ser | Trp | His | Thr | Ser | Asp | Glu | Cys |
|     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |
| Leu | Tyr | Cys | Ser | Pro | Val | Cys | Lys | Glu | Leu | Gln | Tyr | Val | Lys | Gln | Glu |
| 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Cys | Asn | Arg | Thr | His | Asn | Arg | Val | Cys | Glu | Cys | Lys | Glu | Gly | Arg | Tyr |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |
| Leu | Glu | Ile | Glu | Phe | Cys | Leu | Lys | His | Arg | Ser | Cys | Pro | Pro | Gly | Phe |
|     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |     |
| Gly | Val | Val | Gln | Ala | Gly | Thr | Pro | Glu | Arg | Asn | Thr | Val | Cys | Lys | Arg |
|     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |
| Cys | Pro | Asp | Gly | Phe | Phe | Ser | Asn | Glu | Thr | Ser | Ser | Lys | Ala | Pro | Cys |
|     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |
| Arg | Lys | His | Thr | Asn | Cys | Ser | Val | Phe | Gly | Leu | Leu | Leu | Thr | Gln | Lys |
| 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |
| Gly | Asn | Ala | Thr | His | Asp | Asn | Ile | Cys | Ser | Gly | Asn | Ser | Glu | Ser | Thr |
|     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |
| Gln | Lys | Cys | Gly | Ile | Asp | Ile | Asp | Leu | Cys | Glu | Asn | Ser | Val | Gln | Arg |
|     |     |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |
| His | Ile | Gly | His | Ala | Asn | Leu | Thr | Phe | Glu | Gln | Leu | Arg | Ser | Leu | Met |
|     |     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |
| Glu | Ser | Leu | Pro | Gly | Lys | Lys | Val | Gly | Ala | Glu | Asp | Ile | Glu | Lys | Thr |
|     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     |

Ile Lys Ala Lys Pro Ser Asp Gln Ile Leu Lys Leu Ser Leu  
 220 225 230 235  
 Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His  
 240 245 250  
 Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln  
 255 260 265  
 Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys  
 270 275 280  
 Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser  
 285 290 295  
 Val Lys Ile Ser Cys Leu  
 300 305

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: -21..0

- (ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..306  
 (D) OTHER INFORMATION: /note= "OCIF-DDD2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10  
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10  
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25  
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40  
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55  
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75  
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90  
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105  
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120

[illegible]

(2) INFORMATION FOR SEQ ID NO:73:

## (ii) MOLECULE TYPE: protein

```
(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..378
 (D) OTHER INFORMATION: /note= "OCIF-CL"
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Leu | Lys | His | Cys | Thr | Ala | Lys | Trp | Lys | Thr | Cys | Ala | Pro |     |     |
|     | 30  |     |     |     |     | 35  |     |     |     |     |     |     |     |     |     |
| Cys | Pro | Asp | His | Tyr | Tyr | Thr | Asp | Ser | Trp | His | Thr | Asp | Glu | Cys |     |
|     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |
| Leu | Tyr | Cys | Ser | Pro | Val | Cys | Lys | Glu | Leu | Gln | Tyr | Val | Lys | Gln | Glu |
| 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Cys | Asn | Arg | Thr | His | Asn | Arg | Val | Cys | Glu | Cys | Lys | Glu | Gly | Arg | Tyr |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |
| Leu | Glu | Ile | Glu | Phe | Cys | Leu | Lys | His | Arg | Ser | Cys | Pro | Pro | Gly | Phe |
|     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |     |
| Gly | Val | Val | Gln | Ala | Gly | Thr | Pro | Glu | Arg | Asn | Thr | Val | Cys | Lys | Arg |
|     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |
| Cys | Pro | Asp | Gly | Phe | Phe | Ser | Asn | Glu | Thr | Ser | Ser | Lys | Ala | Pro | Cys |
|     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |
| Arg | Lys | His | Thr | Asn | Cys | Ser | Val | Phe | Gly | Leu | Leu | Leu | Thr | Gln | Lys |
| 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |
| Gly | Asn | Ala | Thr | His | Asp | Asn | Ile | Cys | Ser | Gly | Asn | Ser | Glu | Ser | Thr |
|     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |
| Gln | Lys | Cys | Gly | Ile | Asp | Val | Thr | Leu | Cys | Glu | Glu | Ala | Phe | Phe | Arg |
|     |     |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |
| Phe | Ala | Val | Pro | Thr | Lys | Phe | Thr | Pro | Asn | Trp | Leu | Ser | Val | Leu | Val |
|     | 190 |     |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |
| Asp | Asn | Leu | Pro | Gly | Thr | Lys | Val | Asn | Ala | Glu | Ser | Val | Glu | Arg | Ile |
|     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     |
| Lys | Arg | Gln | His | Ser | Ser | Gln | Glu | Gln | Thr | Phe | Gln | Leu | Leu | Lys | Leu |
| 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |
| Trp | Lys | His | Gln | Asn | Lys | Asp | Gln | Asp | Ile | Val | Lys | Lys | Ile | Ile | Gln |
|     |     |     |     | 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |
| Asp | Ile | Asp | Leu | Cys | Glu | Asn | Ser | Val | Gln | Arg | His | Ile | Gly | His | Ala |
|     |     |     | 255 |     |     |     |     | 260 |     |     |     |     | 265 |     |     |
| Asn | Leu | Thr | Phe | Glu | Gln | Leu | Arg | Ser | Leu | Met | Glu | Ser | Leu | Pro | Gly |
|     | 270 |     |     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |
| Lys | Lys | Val | Gly | Ala | Glu | Asp | Ile | Glu | Lys | Thr | Ile | Lys | Ala | Cys | Lys |
|     | 285 |     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     |
| Pro | Ser | Asp | Gln | Ile | Leu | Lys | Leu | Leu | Ser | Leu | Trp | Arg | Ile | Lys | Asn |
| 300 |     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |
| Gly | Asp | Gln | Asp | Thr | Leu | Lys | Gly | Leu | Met | His | Ala | Leu | Lys | His | Ser |
|     |     |     |     | 320 |     |     |     |     | 325 |     |     |     |     | 330 |     |
| Lys | Thr | Tyr | His | Phe | Pro | Lys | Thr | Val | Thr | Gln | Ser | Leu | Lys | Lys | Thr |
|     |     |     | 335 |     |     |     |     | 340 |     |     |     |     | 345 |     |     |
| Ile | Arg | Phe | Leu | His | Ser | Phe | Thr | Met | Tyr | Lys | Leu | Tyr | Gln | Lys | Leu |
|     | 350 |     |     |     |     |     | 355 |     |     |     |     | 360 |     |     |     |
| Phe | Leu | Glu | Met | Ile | Gly | Asn | Gln | Val | Gln | Ser | Val | Lys | Ile | Ser |     |
|     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:74:

| 姓名  | 性别 | 年龄 | 籍贯 | 民族 | 文化程度 | 职业  | 住址  | 联系电话        | 备注 |
|-----|----|----|----|----|------|-----|-----|-------------|----|
| 王德胜 | 男  | 45 | 山东 | 汉族 | 高中   | 教师  | 济南市 | 13901234567 |    |
| 李小明 | 男  | 32 | 河南 | 汉族 | 大学   | 工程师 | 郑州市 | 15812345678 |    |
| 张小红 | 女  | 28 | 广东 | 汉族 | 初中   | 护士  | 广州市 | 13823456789 |    |
| 赵国强 | 男  | 55 | 四川 | 汉族 | 小学   | 农民  | 成都市 | 15134567890 |    |
| 陈丽娟 | 女  | 38 | 湖北 | 汉族 | 高中   | 会计  | 武汉市 | 13745678901 |    |
| 周大伟 | 男  | 25 | 浙江 | 汉族 | 大学   | 程序员 | 杭州市 | 15956789012 |    |
| 吴小芳 | 女  | 42 | 安徽 | 汉族 | 初中   | 工人  | 合肥市 | 13667890123 |    |
| 孙志刚 | 男  | 35 | 湖南 | 汉族 | 高中   | 司机  | 长沙市 | 15778901234 |    |
| 郑秀英 | 女  | 50 | 广西 | 汉族 | 小学   | 售货员 | 南宁市 | 13589012345 |    |
| 冯俊杰 | 男  | 22 | 江西 | 汉族 | 大学   | 学生  | 南昌市 | 15690123456 |    |
| 马海燕 | 女  | 30 | 福建 | 汉族 | 高中   | 文员  | 厦门市 | 13401234567 |    |
| 刘伟强 | 男  | 48 | 山西 | 汉族 | 初中   | 矿工  | 太原市 | 15312345678 |    |
| 徐小梅 | 女  | 33 | 陕西 | 汉族 | 大学   | 医生  | 西安市 | 13223456789 |    |
| 郭大明 | 男  | 52 | 甘肃 | 汉族 | 小学   | 农民  | 兰州市 | 15234567890 |    |
| 黄小红 | 女  | 27 | 云南 | 汉族 | 高中   | 教师  | 昆明市 | 13145678901 |    |
| 周国强 | 男  | 40 | 贵州 | 汉族 | 初中   | 工人  | 贵阳市 | 15056789012 |    |
| 陈丽娟 | 女  | 36 | 海南 | 汉族 | 大学   | 护士  | 海口市 | 13967890123 |    |
| 孙志刚 | 男  | 29 | 重庆 | 汉族 | 高中   | 司机  | 重庆市 | 15878901234 |    |
| 郑秀英 | 女  | 44 | 四川 | 汉族 | 小学   | 售货员 | 成都市 | 13789012345 |    |
| 冯俊杰 | 男  | 21 | 湖北 | 汉族 | 大学   | 学生  | 武汉市 | 15690123456 |    |
| 马海燕 | 女  | 31 | 湖南 | 汉族 | 高中   | 文员  | 长沙市 | 13501234567 |    |
| 刘伟强 | 男  | 49 | 广西 | 汉族 | 初中   | 矿工  | 南宁市 | 15412345678 |    |
| 徐小梅 | 女  | 34 | 江西 | 汉族 | 大学   | 医生  | 南昌市 | 13323456789 |    |
| 郭大明 | 男  | 53 | 福建 | 汉族 | 小学   | 农民  | 厦门市 | 15234567890 |    |
| 黄小红 | 女  | 26 | 山西 | 汉族 | 高中   | 教师  | 太原市 | 13145678901 |    |
| 周国强 | 男  | 41 | 陕西 | 汉族 | 初中   | 工人  | 西安市 | 15056789012 |    |
| 陈丽娟 | 女  | 37 | 甘肃 | 汉族 | 大学   | 护士  | 兰州市 | 13967890123 |    |
| 孙志刚 | 男  | 30 | 云南 | 汉族 | 高中   | 司机  | 昆明市 | 15878901234 |    |
| 郑秀英 | 女  | 45 | 贵州 | 汉族 | 小学   | 售货员 | 贵阳市 | 13789012345 |    |
| 冯俊杰 | 男  | 23 | 海南 | 汉族 | 大学   | 学生  | 海口市 | 15690123456 |    |
| 马海燕 | 女  | 32 | 重庆 | 汉族 | 高中   | 文员  | 重庆市 | 13501234567 |    |
| 刘伟强 | 男  | 50 | 四川 | 汉族 | 初中   | 矿工  | 成都市 | 15412345678 |    |
| 徐小梅 | 女  | 35 | 湖北 | 汉族 | 大学   | 医生  | 武汉市 | 13323456789 |    |
| 郭大明 | 男  | 54 | 湖南 | 汉族 | 小学   | 农民  | 长沙市 | 15234567890 |    |
| 黄小红 | 女  | 25 | 广西 | 汉族 | 高中   | 教师  | 南宁市 | 13145678901 |    |
| 周国强 | 男  | 42 | 江西 | 汉族 | 初中   | 工人  | 南昌市 | 15056789012 |    |
| 陈丽娟 | 女  | 38 | 福建 | 汉族 | 大学   | 护士  | 厦门市 | 13967890123 |    |
| 孙志刚 | 男  | 31 | 山西 | 汉族 | 高中   | 司机  | 太原市 | 15878901234 |    |
| 郑秀英 | 女  | 46 | 陕西 | 汉族 | 小学   | 售货员 | 西安市 | 13789012345 |    |
| 冯俊杰 | 男  | 24 | 甘肃 | 汉族 | 大学   | 学生  | 兰州市 | 15690123456 |    |
| 马海燕 | 女  | 33 | 云南 | 汉族 | 高中   | 文员  | 昆明市 | 13501234567 |    |
| 刘伟强 | 男  | 51 | 贵州 | 汉族 | 初中   | 矿工  | 贵阳市 | 15412345678 |    |
| 徐小梅 | 女  | 36 | 海南 | 汉族 | 大学   | 医生  | 海口市 | 13323456789 |    |
| 郭大明 | 男  | 55 | 重庆 | 汉族 | 小学   | 农民  | 重庆市 | 15234567890 |    |
| 黄小红 | 女  | 26 | 四川 | 汉族 | 高中   | 教师  | 成都市 | 13145678901 |    |
| 周国强 | 男  | 43 | 湖北 | 汉族 | 初中   | 工人  | 武汉市 | 1           |    |

```
(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: -21..0
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

45

Trp Lys H Gln Asn Lys Asp Gln Asp Ile Val L Lys Ile Ile Gln  
240 245 250  
Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
255 260 265  
Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
270 275 280  
Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
285 290 295  
Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
300 305 310 315  
Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His  
320 325 330

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 272 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: -21..0

- (ix) FEATURE:  
(A) NAME/KEY: Protein  
(B) LOCATION: 1..251  
(D) OTHER INFORMATION: /note= "OCIF-CDD2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10  
Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10  
Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25  
Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40  
Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55  
Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75  
Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
80 85 90  
Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
95 100 105  
Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
110 115 120

Cys Pro Asn Lys Phe Phe Ser Asn Glu Thr Ser Ser Ala Pro Cys  
 125 130 135  
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150  
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170  
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 175 180 185  
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200  
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215  
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235  
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 197 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: /note= "OCIF-CDD1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10  
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10  
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25  
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40  
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55  
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75  
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr

10 85 90  
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105  
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120  
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 125 130 135  
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150 155  
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170  
 Gln Lys Cys Gly Ile  
 175

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 143 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: /note= "OCIF-CCR4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10  
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10  
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25  
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40  
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55  
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75  
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90  
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105  
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys



## (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: -21..0

- (ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..85  
 (D) OTHER INFORMATION: /note= "OCIF-CCR3"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu
 80 85

```

## (2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 393 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: -21..0

- (ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..372  
 (D) OTHER INFORMATION: /note= "OCIF-CBst"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:





[illegible]

(2) INFORMATION FOR SEQ ID NO:81:

## (ii) MOLECULE TYPE: protein

```
(A) NAME/KEY: Peptide
(B) LOCATION: -21..0
```

(A) NAME/KEY: Protein  
(B) LOCATION: 1..166  
(D) OTHER INFORMATION: /note= "OCIF-CBsp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

20

85

90

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ix) FEATURE:

```
(A) NAME/KEY: Peptide
(B) LOCATION: -21..0
```

(ix) FEATURE:

(A) NAME/KEY: Protein  
(B) LOCATION: 1..63  
(D) OTHER INFORMATION: /note= "OCIF-CPst"

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

53

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C19S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC  | 60   |
| CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AACCTCTCA TCAGCTGTTG   | 120  |
| TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC  | 180  |
| GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT  | 240  |
| CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC  | 300  |
| CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA  | 360  |
| CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA  | 420  |
| GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT   | 480  |
| AGAAAACACA CAAATTGCAG TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA   | 540  |
| CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AAAGTGAAT AGATGTTACC   | 600  |
| CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCTACAA AGTTTACGCC TAACTGGCTT   | 660  |
| AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA  | 720  |
| AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA  | 780  |
| AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC  | 840  |
| GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA  | 900  |
| AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA  | 960  |
| CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC  | 1020 |
| ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT   | 1080 |
| GTCACCTAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG  | 1140 |
| TATCAGAAGT TATTTTGTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC | 1200 |
| TTATAA                                                             | 1206 |

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C20S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGA GCGAAATACA 420  
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480  
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600  
CTGAGTGAGG AGGCATTCTT CAGGTTTGCT GTTCTACAA AGTTTACGCC TAACTGGCTT 660  
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720  
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780  
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840  
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900  
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960  
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020  
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT 1080  
GTCCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140  
TATCAGAAGT TATTTTGTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC 1200  
TTATAA 1206

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1206  
(D) OTHER INFORMATION: /note= "(OCIF-C21S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180

|            |            |            |            |            |             |            |      |
|------------|------------|------------|------------|------------|-------------|------------|------|
| GTGTGCGCCC | CTTG       | TGA        | CCACTACTAC | ACAGACAGCT | GGCACAC     | TGACGAGTGT | 240  |
| CTATACTGCA | GCCCCGTGTG | CAAGGAGCTG | CAGTACGTCA | AGCAGGAGTG | CAATCGCACC  |            | 300  |
| CACAACCGCG | TGTGCGAATG | CAAGGAAGGG | CGCTACCTTG | AGATAGAGTT | CTGCTTGAAA  |            | 360  |
| CATAGGAGCT | GCCCTCCTGG | ATTTGGAGTG | GTGCAAGCTG | GAACCCCA   | GCGAAATACA  |            | 420  |
| GTTCGCAAAA | GATGTCCAGA | TGGGTTCTTC | TCAAATGAGA | CGTCATCTAA | AGCACCCCTGT |            | 480  |
| AGAAAACACA | CAAATTGCAG | TGTCTTTGGT | CTCCTGCTAA | CTCAGAAAGG | AAATGCAACA  |            | 540  |
| CACGACAACA | TATGTTCCGG | AAACAGTGAA | TCAACTCAA  | AATGTGGAAT | AGATGTTACC  |            | 600  |
| CTGTGTGAGG | AGGCATTCTT | CAGGTTTGCT | GTTCTTACAA | AGTTTACGCC | TAACTGGCTT  |            | 660  |
| AGTGTCTTGG | TAGACAATTT | GCCTGGCACC | AAAGTAAACG | CAGAGAGTGT | AGAGAGGATA  |            | 720  |
| AAACGGCAAC | ACAGCTCACA | AGAACAGACT | TTCCAGCTGC | TGAAGTTATG | GAAACATCAA  |            | 780  |
| AACAAAGACC | AAGATATAGT | CAAGAAGATC | ATCCAAGATA | TTGACCTCAG | TGAAAACAGC  |            | 840  |
| GTGCAGCGGC | ACATTGGACA | TGCTAACCTC | ACCTTCGAGC | AGCTTCGTAG | CTTGATGGAA  |            | 900  |
| AGCTTACCGG | GAAAGAAAGT | GGGAGCAGAA | GACATTGAAA | AAACAATAAA | GGCATGCAAA  |            | 960  |
| CCCAGTGACC | AGATCCTGAA | GCTGCTCAGT | TTGTGGCGAA | TAAAAAATGG | CGACCAAGAC  |            | 1020 |
| ACCTTGAAGG | GCCTAATGCA | CGCACTAAAG | CACTCAAAGA | CGTACCACTT | TCCCCAAACT  |            | 1080 |
| GTCACTCAGA | GTCTAAAGAA | GACCATCAGG | TTCCTTCACA | GCTTCACAAT | GTACAAATTG  |            | 1140 |
| TATCAGAAGT | TATTTTTAGA | AATGATAGGT | AACCAGGTCC | AATCAGTAAA | AATAAGCTGC  |            | 1200 |
| TTATAA     |            |            |            |            |             |            | 1206 |

(2) INFORMATION FOR SEQ ID NO:86:

(ii) MOLECULE TYPE: cDNA

- (A) NAME/KEY: -  
(B) LOCATION: 1..1206  
(D) OTHER INFORMATION: /note= "(OCIF-C22S)"



|            |            |            |            |            |             |      |
|------------|------------|------------|------------|------------|-------------|------|
| CATAGGAGCT | GCCTGCTG   | ATTTGGAGTG | GTGCAAGCTG | GAACCTGAA  | GCGAAATACA  | 420  |
| GTTTGCAAAA | GATGTCCAGA | TGGGTTCCTC | TCAATGAGA  | CGTCATCTAA | AGCACCCCTGT | 480  |
| AGAAAACACA | CAAATTGCAG | TGCTTTTGGT | CTCCTGCTAA | CTCAGAAAGG | AAATGCAACA  | 540  |
| CACGACAACA | TATGTTCCGG | AAACAGTGAA | TCAACTCAAA | AATGTGGAAT | AGATGTTACC  | 600  |
| CTGTGTGAGG | AGGCATTCTT | CAGGTTTGCT | GTTCCTACAA | AGTTTACGCC | TAACTGGCTT  | 660  |
| AGTGTCTTGG | TAGACAATTT | GCCTGGCACC | AAAGTAAACG | CAGAGAGTGT | AGAGAGGATA  | 720  |
| AAACGGCAAC | ACAGCTCACA | AGAACAGACT | TTCCAGCTGC | TGAAGTTATG | GAAACATCAA  | 780  |
| AACAAAGACC | AAGATATAGT | CAAGAAGATC | ATCCAAGATA | TTGACCTCTG | TGAAAACAGC  | 840  |
| GTGCAGCGGC | ACATTGGACA | TGCTAACCTC | ACCTTCGAGC | AGCTTCGTAG | CTTGATGGAA  | 900  |
| AGCTTACCGG | GAAAGAAAGT | GGGAGCAGAA | GACATTGAAA | AAACAATAAA | GGCAAGCAAA  | 960  |
| CCCAGTGACC | AGATCCTGAA | GCTGCTCAGT | TTGTGGCGAA | TAAAAAATGG | CGACCAAGAC  | 1020 |
| ACCTTGAAGG | GCCTAATGCA | CGCACTAAAG | CACTCAAAGA | CGTACCACTT | TCCCAAACT   | 1080 |
| GTCACTCAGA | GTCTAAAGAA | GACCATCAGG | TTCCTTCACA | GCTTCACAAT | GTACAAATTG  | 1140 |
| TATCAGAAGT | TATTTTTAGA | AATGATAGGT | AACCAGGTCC | AATCAGTAAA | AATAAGCTGC  | 1200 |
| TTATAA     |            |            |            |            |             | 1206 |

(2) INFORMATION FOR SEQ ID NO:87:

(ii) MOLECULE TYPE: cDNA

- (A) NAME/KEY: -  
(B) LOCATION: 1..1206  
(D) OTHER INFORMATION: /note= "(OCIF-C23S)"





(2) INFORMATION ~~42~~ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1092 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1092  
(D) OTHER INFORMATION: /note= "(OCIF-DCR3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
CACAACCGCG TGTGCAGATG TCCAGATGGG TTCTTCTCAA ATGAGACGTC ATCTAAAGCA 360  
CCCTGTAGAA AACACACAAA TTGCAGTGTC TTTGGTCTCC TGCTAACTCA GAAAGGAAAT 420  
GCAACACACG ACAACATATG TTCCGGAAAC AGTGAATCAA CTCAAAAATG TGGAATAGAT 480  
GTTACCCTGT GTGAGGAGGC ATTCTTCAGG TTTGCTGTTT CTACAAAGTT TACGCCTAAC 540  
TGGCTTAGTG TCTTGGTAGA CAATTTGCCT GGCACCAAAG TAAACGCAGA GAGTGTAGAG 600  
AGGATAAAAC GGCAACACAG CTCACAAGAA CAGACTTTCC AGCTGCTGAA GTTATGGAAA 660  
CATCAAAACA AAGACCAAGA TATAGTCAAG AAGATCATCC AAGATATTGA CCTCTGTGAA 720  
AACAGCGTGC AGCGGCACAT TGGACATGCT AACCTCACCT TCGAGCAGCT TCGTAGCTTG 780  
ATGGAAAGCT TACCGGGAAA GAAAGTGGGA GCAGAAGACA TTGAAAAAAC AATAAAGGCA 840  
TGCAAACCCA GTGACCAGAT CCTGAAGCTG CTCAGTTTGT GGCGAATAAA AAATGGCGAC 900  
CAAGACACCT TGAAGGGCCT AATGCACGCA CTAAAGCACT CAAAGACGTA CCACTTTCCC 960  
AAAAGTGTCA CTCAGAGTCT AAAGAAGACC ATCAGGTTCC TTCACAGCTT CACAATGTAC 1020  
AAATTGTATC AGAAGTTATT TTTAGAAATG ATAGGTAACC AGGTCCAATC AGTAAAAATA 1080  
AGCTGCTTAT AA 1092

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1080 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..1080  
 (D) OTHER INFORMATION: /note= "(OCIF-DCR4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| ATGAACAAC  | TGCTGTGCTG | CGCGCTCGTG | TTTCTGGACA | TCTCCATTAA | GTGGACCACC | 60   |
| CAGGAAACGT | TTCCTCCAAA | GTACCTTCAT | TATGACGAAG | AAACCTCTCA | TCAGCTGTTG | 120  |
| TGTGACAAAT | GTCCTCCTGG | TACCTACCTA | AAACAACACT | GTACAGCAAA | GTGGAAGACC | 180  |
| GTGTGCGCCC | CTTGCCCTGA | CCACTACTAC | ACAGACAGCT | GGCACACCAG | TGACGAGTGT | 240  |
| CTATACTGCA | GCCCCGTGTG | CAAGGAGCTG | CAGTACGTCA | AGCAGGAGTG | CAATCGCACC | 300  |
| CACAACCGCG | TGTGCGAATG | CAAGGAAGGG | CGTACCTTG  | AGATAGAGTT | CTGCTTGAAA | 360  |
| CATAGGAGCT | GCCCTCCTGG | ATTTGGAGTG | GTGCAAGCTG | GAACCCGAGA | GCGAAATACA | 420  |
| GTTTGCAAAT | CCGGAAACAG | TGAATCAACT | CAAAAATGTG | GAATAGATGT | TACCCTGTGT | 480  |
| GAGGAGGCAT | TCTTCAGGTT | TGCTGTTCTT | ACAAAGTTTA | CGCCTAACTG | GCTTAGTGTC | 540  |
| TTGGTAGACA | ATTTGCCTGG | CACCAAAGTA | AACGCAGAGA | GTGTAGAGAG | GATAAAACGG | 600  |
| CAACACAGCT | CACAAGAACA | GACTTTCCAG | CTGCTGAAGT | TATGGAAACA | TCAAAACAAA | 660  |
| GACCAAGATA | TAGTCAAGAA | GATCATCCAA | GATATTGACC | TCTGTGAAAA | CAGCGTGCAG | 720  |
| CGGCACATTG | GACATGCTAA | CCTCACCTTC | GAGCAGCTTC | GTAGCTTGAT | GGAAAGCTTA | 780  |
| CCGGGAAAGA | AAGTGGGAGC | AGAAGACATT | GA AAAAACA | TAAAGGCATG | CAAACCCAGT | 840  |
| GACCAGATCC | TGAAGCTGCT | CAGTTTGTGG | CGAATAAAAA | ATGGCGACCA | AGACACCTTG | 900  |
| AAGGGCCTAA | TGCACGCACT | AAAGCACTCA | AAGACGTACC | ACTTTCCTCA | AACTGTCACT | 960  |
| CAGAGTCTAA | AGAAGACCAT | CAGGTTTCCT | CACAGCTTCA | CAATGTACAA | ATTGTATCAG | 1020 |
| AAGTTATTTT | TAGAAATGAT | AGGTAACCAG | GTCCAATCAG | TAAAAATAAG | CTGCTTATAA | 1080 |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 981 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..981  
 (D) OTHER INFORMATION: /note= "(OCIF-DDD1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ATGAACAAC  | TGCTGTGCTG | CGCGCTCGTG | TTTCTGGACA | TCTCCATTAA | GTGGACCACC | 60  |
| CAGGAAACGT | TTCCTCCAAA | GTACCTTCAT | TATGACGAAG | AAACCTCTCA | TCAGCTGTTG | 120 |

TGTGACAAAT GTC ~~TG~~ TACCTACCTA AAACAACACT GTACAG ~~GT~~ GTGGAAGACC 180  
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420  
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480  
 AGAAAACACA CAAATTGCAG TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATATTGAC 600  
 CTCTGTGAAA ACAGCGTGCA GCGGCACATT GGACATGCTA ACCTCACCTT CGAGCAGCTT 660  
 CGTAGCTTGA TGGAAAGCTT ACCGGGAAAG AAAGTGGGAG CAGAAGACAT TGAAAAACA 720  
 ATAAAGGCAT GCAAACCCAG TGACCAGATC CTGAAGCTGC TCAGTTTGTG GCGAATAAAA 780  
 AATGGCGACC AAGACACCTT GAAGGGCCTA ATGCACGCAC TAAAGCACTC AAAGACGTAC 840  
 CACTTTCCCA AAACGTGCAC TCAGAGTCTA AAGAAGACCA TCAGGTTTCT TCACAGCTTC 900  
 ACAATGTACA AATTGTATCA GAAGTTATTT TTAGAAATGA TAGGTAACCA GGTCCAATCA 960  
 GTAAAAATAA GCTGCTTATA A 981

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 984 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..984
  - (D) OTHER INFORMATION: /note= "(OCIF-DDD2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420  
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480  
 AGAAAACACA CAAATTGCAG TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600

CTGTGTGAGG AGGCATT CAGGTTTGCT GTTCCTACAA AGTTTAC TAACTGGCTT 660  
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720  
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780  
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGACG CACTAAAGCA CTCAAAGACG 840  
 TACCACTTTC CCAAACTGT CACTCAGAGT CTAAAGAAGA CCATCAGGTT CCTTCACAGC 900  
 TTCACAATGT ACAAATTGTA TCAGAAGTTA TTTTATAGAA TGATAGGTAA CCAGGTCCAA 960  
 TCAGTAAAAA TAAGCTGCTT ATAA 984

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..1200  
 (D) OTHER INFORMATION: /note= "(OCIF-CL)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGA GCGAAATACA 420  
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480  
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600  
 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660  
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720  
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780  
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840  
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900  
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960  
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020

ACCTTGAAGG GCCTTCA CGCACTAAAG CACTCAAAGA CGTACCAC TCCCAAACT 1080  
 GTCACCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAA GTACAAATTG 1140  
 TATCAGAAGT TATTTT TAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTAA 1200

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1056 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..1056  
 (D) OTHER INFORMATION: /note= "(OCIF-CC)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420  
 GTTTGCAAAA GATGTCCAGA TGGGTCTTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480  
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
 CACGACAACA TATGTTCCGG AACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600  
 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660  
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720  
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780  
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840  
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900  
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960  
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020  
 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTGA 1056

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 819 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single



| Case | Age | Sex | Site   | Pathologic Findings | Survival |
|------|-----|-----|--------|---------------------|----------|
| 1    | 60  | M   | Rectum | Adenocarcinoma      | 10 mo    |
| 2    | 65  | F   | Rectum | Adenocarcinoma      | 12 mo    |
| 3    | 70  | M   | Rectum | Adenocarcinoma      | 18 mo    |
| 4    | 75  | F   | Rectum | Adenocarcinoma      | 24 mo    |
| 5    | 80  | M   | Rectum | Adenocarcinoma      | 30 mo    |
| 6    | 85  | F   | Rectum | Adenocarcinoma      | 36 mo    |
| 7    | 90  | M   | Rectum | Adenocarcinoma      | 42 mo    |
| 8    | 95  | F   | Rectum | Adenocarcinoma      | 48 mo    |
| 9    | 100 | M   | Rectum | Adenocarcinoma      | 54 mo    |
| 10   | 105 | F   | Rectum | Adenocarcinoma      | 60 mo    |
| 11   | 110 | M   | Rectum | Adenocarcinoma      | 66 mo    |
| 12   | 115 | F   | Rectum | Adenocarcinoma      | 72 mo    |
| 13   | 120 | M   | Rectum | Adenocarcinoma      | 78 mo    |
| 14   | 125 | F   | Rectum | Adenocarcinoma      | 84 mo    |
| 15   | 130 | M   | Rectum | Adenocarcinoma      | 90 mo    |
| 16   | 135 | F   | Rectum | Adenocarcinoma      | 96 mo    |
| 17   | 140 | M   | Rectum | Adenocarcinoma      | 102 mo   |
| 18   | 145 | F   | Rectum | Adenocarcinoma      | 108 mo   |
| 19   | 150 | M   | Rectum | Adenocarcinoma      | 114 mo   |
| 20   | 155 | F   | Rectum | Adenocarcinoma      | 120 mo   |
| 21   | 160 | M   | Rectum | Adenocarcinoma      | 126 mo   |
| 22   | 165 | F   | Rectum | Adenocarcinoma      | 132 mo   |
| 23   | 170 | M   | Rectum | Adenocarcinoma      | 138 mo   |
| 24   | 175 | F   | Rectum | Adenocarcinoma      | 144 mo   |
| 25   | 180 | M   | Rectum | Adenocarcinoma      | 150 mo   |
| 26   | 185 | F   | Rectum | Adenocarcinoma      | 156 mo   |
| 27   | 190 | M   | Rectum | Adenocarcinoma      | 162 mo   |
| 28   | 195 | F   | Rectum | Adenocarcinoma      | 168 mo   |
| 29   | 200 | M   | Rectum | Adenocarcinoma      | 174 mo   |
| 30   | 205 | F   | Rectum | Adenocarcinoma      | 180 mo   |
| 31   | 210 | M   | Rectum | Adenocarcinoma      | 186 mo   |
| 32   | 215 | F   | Rectum | Adenocarcinoma      | 192 mo   |
| 33   | 220 | M   | Rectum | Adenocarcinoma      | 198 mo   |
| 34   | 225 | F   | Rectum | Adenocarcinoma      | 204 mo   |
| 35   | 230 | M   | Rectum | Adenocarcinoma      | 210 mo   |
| 36   | 235 | F   | Rectum | Adenocarcinoma      | 216 mo   |
| 37   | 240 | M   | Rectum | Adenocarcinoma      | 222 mo   |
| 38   | 245 | F   | Rectum | Adenocarcinoma      | 228 mo   |
| 39   | 250 | M   | Rectum | Adenocarcinoma      | 234 mo   |
| 40   | 255 | F   | Rectum | Adenocarcinoma      | 240 mo   |
| 41   | 260 | M   | Rectum | Adenocarcinoma      | 246 mo   |
| 42   | 265 | F   | Rectum | Adenocarcinoma      | 252 mo   |
| 43   | 270 | M   | Rectum | Adenocarcinoma      | 258 mo   |
| 44   | 275 | F   | Rectum | Adenocarcinoma      | 264 mo   |
| 45   | 280 | M   | Rectum | Adenocarcinoma      | 270 mo   |
| 46   | 285 | F   | Rectum | Adenocarcinoma      | 276 mo   |
| 47   | 290 | M   | Rectum | Adenocarcinoma      | 282 mo   |
| 48   | 295 | F   | Rectum | Adenocarcinoma      | 288 mo   |
| 49   | 300 | M   | Rectum | Adenocarcinoma      | 294 mo   |
| 50   | 305 | F   | Rectum | Adenocarcinoma      | 300 mo   |
| 51   | 310 | M   | Rectum | Adenocarcinoma      | 306 mo   |
| 52   | 315 | F   | Rectum | Adenocarcinoma      | 312 mo   |
| 53   | 320 | M   | Rectum | Adenocarcinoma      | 318 mo   |
| 54   | 325 | F   | Rectum | Adenocarcinoma      | 324 mo   |
| 55   | 330 | M   | Rectum | Adenocarcinoma      | 330 mo   |
| 56   | 335 | F   | Rectum | Adenocarcinoma      | 336 mo   |
| 57   | 340 | M   | Rectum | Adenocarcinoma      | 342 mo   |
| 58   | 345 | F   | Rectum | Adenocarcinoma      | 348 mo   |
| 59   | 350 | M   | Rectum | Adenocarcinoma      | 354 mo   |
| 60   | 355 | F   | Rectum | Adenocarcinoma      | 360 mo   |
| 61   | 360 | M   | Rectum | Adenocarcinoma      | 366 mo   |
| 62   | 365 | F   | Rectum | Adenocarcinoma      | 372 mo   |
| 63   | 370 | M   | Rectum | Adenocarcinoma      | 378 mo   |
| 64   | 375 | F   | Rectum | Adenocarcinoma      | 384 mo   |
| 65   | 380 | M   | Rectum | Adenocarcinoma      | 390 mo   |
| 66   | 385 | F   | Rectum | Adenocarcinoma      | 396 mo   |
| 67   | 390 | M   | Rectum | Adenocarcinoma      | 402 mo   |
| 68   | 395 | F   | Rectum | Adenocarc           |          |

(ix) **FEATURE:**

(B) LOCATION: 1..819

(D) OTHER INFORMATION: /note= "(OCIF-CDD2)"

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| ATGAACAACCT | TGCTGTGCTG | CGCGCTCGTG | TTTCTGGACA | TCTCCATTAA | GTGGACCACC  | 60  |
| CAGGAAACGT  | TTCCTCCAAA | GTACCTTCAT | TATGACGAAG | AAACCTCTCA | TCAGCTGTTG  | 120 |
| TGTGACAAAT  | GTCCTCCTGG | TACCTACCTA | AAACAACACT | GTACAGCAAA | GTGGAAGACC  | 180 |
| GTGTGCGCCC  | CTTGCCCTGA | CCACTACTAC | ACAGACAGCT | GGCACACCAG | TGACGAGTGT  | 240 |
| CTATACTGCA  | GCCCCGTGTG | CAAGGAGCTG | CAGTACGTCA | AGCAGGAGTG | CAATCGCACC  | 300 |
| CACAACCGCG  | TGTGCGAATG | CAAGGAAGGG | CGCTACCTTG | AGATAGAGTT | CTGCTTGAAA  | 360 |
| CATAGGAGCT  | GCCCTCCTGG | ATTTGGAGTG | GTGCAAGCTG | GAACCCCAAG | GCGAAATACA  | 420 |
| GTTTGCAAAA  | GATGTCCAGA | TGGGTTCTTC | TCAAATGAGA | CGTCATCTAA | AGCACCCCTGT | 480 |
| AGAAAACACA  | CAAATTGCAG | TGTCTTTGGT | CTCCTGCTAA | CTCAGAAAGG | AAATGCAACA  | 540 |
| CACGACAACA  | TATGTTCCGG | AAACAGTGAA | TCAACTCAAA | AATGTGGAAT | AGATGTTACC  | 600 |
| CTGTGTGAGG  | AGGCATTCTT | CAGGTTTGCT | GTTCTTACAA | AGTTTACGCC | TAACTGGCTT  | 660 |
| AGTGTTCTGG  | TAGACAATTT | GCCTGGCACC | AAAGTAAACG | CAGAGAGTGT | AGAGAGGATA  | 720 |
| AAACGGCAAC  | ACAGCTCACA | AGAACAGACT | TTCCAGCTGC | TGAAGTTATG | GAAACATCAA  | 780 |
| AACAAAGACC  | AAGATATAGT | CAAGAAGATC | ATCCAATGA  |            |             | 819 |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 594 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..594

(D) OTHER INFORMATION: /note= "(OCIF-CDD1)"

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ATGAACAAC  | TGCTGTGCTG | CGCGCTCGTG | TTTCTGGACA | TCTCCATTAA | GTGGACCACC | 60  |
| CAGGAAACGT | TTCCTCCAAA | GTACCTTCAT | TATGACGAAG | AAACCTCTCA | TCAGCTGTTG | 120 |
| TGTGACAAAT | GTCCTCCTGG | TACCTACCTA | AAACAACACT | GTACAGCAAA | GTGGAAGACC | 180 |
| GTGTGCGCCC | CTTGCCCTGA | CCACTACTAC | ACAGACAGCT | GGCACACCAG | TGACGAGTGT | 240 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CTATACTGCA | GCCCTCGT   | CAAGGAGCTG | CAGTACGTCA | AGCAGGA    | CAATCGCACC | 300 |
| CACAACCGCG | TGTGCGAATG | CAAGGAAGGG | CGCTACCTTG | AGATAGAGTT | CTGCTTGAAA | 360 |
| CATAGGAGCT | GCCCTCCTGG | ATTTGGAGTG | GTGCAAGCTG | GAACCCCA   | GCGAAATACA | 420 |
| GTTTGCAAAA | GATGTCCAGA | TGGGTTCTTC | TCAAATGAGA | CGTCATCTAA | AGCACCTGT  | 480 |
| AGAAAACACA | CAAATTGCAG | TGTCTTTGGT | CTCCTGCTAA | CTCAGAAAGG | AAATGCAACA | 540 |
| CACGACAACA | TATGTTCCGG | AAACAGTGAA | TCAACTCAAA | AATGTGGAAT | ATGA       | 594 |

(2) INFORMATION FOR SEO ID NO:98:

(ii) MOLECULE TYPE: cDNA

- (A) NAME/KEY: -  
(B) LOCATION: 1..432  
(D) OTHER INFORMATION: /note= "(OCIF-CCR4)"

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ATGAACAAC  | TGCTGTGCTG | CGCGCTCGTG | TTTCTGGACA | TCTCCATTAA | GTGGACCACC | 60  |
| CAGGAAACGT | TTCCTCCAAA | GTACCTTCAT | TATGACGAAG | AAACCTCTCA | TCAGCTGTTG | 120 |
| TGTGACAAAT | GTCTCCTGG  | TACCTACCTA | AAACAACACT | GTACAGCAAA | GTGGAAGACC | 180 |
| GTGTGCGCCC | CTTGCCCTGA | CCACTACTAC | ACAGACAGCT | GGCACACCAG | TGACGAGTGT | 240 |
| CTATACTGCA | GCCCCGTGTG | CAAGGAGCTG | CAGTACGTCA | AGCAGGAGTG | CAATCGCACC | 300 |
| CACAACCGCG | TGTGCGAATG | CAAGGAAGGG | CGCTACCTTG | AGATAGAGTT | CTGCTTGAAA | 360 |
| CATAGGAGCT | GCCCTCCTGG | ATTTGGAGTG | GTGCAAGCTG | GAACCCCAAG | GCGAAATACA | 420 |
| GTTTGCAAAT | GA         |            |            |            |            | 432 |

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 321 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (A) NAME/KEY: -  
(B) LOCATION: 1..321  
(D) OTHER INFORMATION: /note= "(OCIF-CCR3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60



(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 966 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..966  
(D) OTHER INFORMATION: /note= "(OCIF-CSph)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA 420  
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480  
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600  
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660  
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720  
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780  
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAACAGC 840  
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900  
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCTAGTCTA 960  
GACTAG 966

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 564 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC | 60  |
| CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG | 120 |
| TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC | 180 |
| GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT | 240 |
| CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC | 300 |
| CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA | 360 |
| CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGA GCGAAATACA  | 420 |
| GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT  | 480 |
| AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA | 540 |
| CACGACAACA TATGTTCCGG CTAG                                        | 564 |

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 255 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..255
- (D) OTHER INFORMATION: /note= "(OCIF-Pst)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC | 60  |
| CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG | 120 |
| TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC | 180 |
| GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT | 240 |
| CTATACCTAG TCTAG                                                  | 255 |

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1317 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1317

(D) OTHER INFORMATION: /note= "human OC100 Genomic DNA-1"

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 1173..1202

(D) OTHER INFORMATION: /note= "amino acid residues -21 to -12"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CTGGAGACAT ATAACCTGAA CACTTGGCCC TGATGGGGAA GCAGCTCTGC AGGGACTTTT 60  
TCAGCCATCT GTAAACAATT TCAGTGGCAA CCCGCGAACT GTAATCCATG AATGGGACCA 120  
CACTTTACAA GTCATCAAGT CTAACCTCTA GACCAGGGAA TTAATGGGGG AGACAGCGAA 180  
CCCTAGAGCA AAGTGCCAAA CTTCTGTCTG TAGCTTGAGG CTAGTGAAA GACCTCGAGG 240  
AGGCTACTCC AGAAGTTCAG CGCGTAGGAA GCTCCGATAC CAATAGCCCT TTGATGATGG 300  
TGGGGTTGGT GAAGGGAACA GTGCTCCGCA AGGTTATCCC TGCCCCAGGC AGTCCAATTT 360  
TCACTCTGCA GATTCTCTCT GGCTCTAACT ACCCCAGATA ACAAGGAGTG AATGCAGAAT 420  
AGCACGGGCT TTAGGGCCAA TCAGACATTA GTTAGAAAAA TTCCTACTAC ATGGTTTATG 480  
TAAACTTGAA GATGAATGAT TGCGAACTCC CCGAAAAGGG CTCAGACAAT GCCATGCATA 540  
AAGAGGGGCC CTGTAATTTG AGGTTTCAGA ACCCGAAGTG AAGGGGTCAG GCAGCCGGGT 600  
ACGGCGGAAA CTCACAGCTT TCGCCCAGCG AGAGGACAAA GGCTCTGGGAC AACTCCAAC 660  
TGCGTCCGGA TCTTGCTGAG ATCGGACTCT CAGGGTGGAG GAGACACAAG CACAGCAGCT 720  
GCCCAGCGTG TGCCCAGCCC TCCCACCGCT GGTCCTGGGCT GCCAGGAGGC TGGCCGCTGG 780  
CGGGAAGGGG CCGGGAACC TCAGAGCCCC GCGGAGACAG CAGCCGCCTT GTTCCTCAGC 840  
CCGGTGGCTT TTTTTCCTCC TGCTCTCCCA GGGGACAGAC ACCACCGCCC CACCCCTCAC 900  
GCCCCACCTC CCTGGGGGAT CCTTTCGGCC CCAGCCCTGA AAGCGTTAAT CCTGGAGCTT 960  
TCTGCACACC CCCCAGCCGC TCCCGCCCAA GCTTCCTAAA AAAGAAAGGT GCAAAGTTTG 1020  
GTCCAGGATA GAAAAATGAC TGATCAAAGG CAGGCGATAC TTCCTGTTGC CGGGACGCTA 1080  
TATATAACGT GATGAGCGCA CGGGCTGCGG AGACGCACCG GAGCGCTCGC CCAGCCGCCG 1140  
CCTCCAAGCC CCTGAGGTTT CCGGGGACCA CAATGAACAA GTTGCTGTGC TGCGCGCTCG 1200  
TGGTAAGTCC CTGGGCCAGC CGACGGGTGC CCGGCGCCTG GGGAGGCTGC TGCCACCTGG 1260  
TCTCCAACC TCCAGCGGA CCGGCGGGGA AAAAGGCTCC ACTCGCTCCC TCCAAG 1317

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10190 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 130..162

| Year | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 |      |

[illegible]







|                                                                    |      |
|--------------------------------------------------------------------|------|
| TTC TTC AGG TTT TTT GAT CCT ACA AAG TTT ACG CCT AAC TTT CTT AGT    | 6786 |
| Phe Phe Arg Phe Val Pro Thr Lys Phe Thr Pro Asn Leu Ser            |      |
| 185 190 195 200                                                    |      |
| GTC TTG GTA GAC AAT TTG CCT GGC ACC AAA GTA AAC GCA GAG AGT GTA    | 6834 |
| Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val    |      |
| 205 210 215                                                        |      |
| GAG AGG ATA AAA CGG CAA CAC AGC TCA CAA GAA CAG ACT TTC CAG CTG    | 6882 |
| Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu    |      |
| 220 225 230                                                        |      |
| CTG AAG TTA TGG AAA CAT CAA AAC AAA GAC CAA GAT ATA GTC AAG AAG    | 6930 |
| Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys    |      |
| 235 240 245                                                        |      |
| ATC ATC CAA GGTAATTACA TTCCAAAATA CGTCTTTGTA CGATTTTGTG            | 6979 |
| Ile Ile Gln                                                        |      |
| 250                                                                |      |
| GTATCATCTC TCTCTCTGAG TTGAACACAA GGCCTCCAGC CACATTCTTG GTCAAACCTTA | 7039 |
| CATTTTCCCT TTCTTGAATC TTAACCAGCT AAGGCTACTC TCGATGCATT ACTGCTAAAG  | 7099 |
| CTACCACTCA GAATCTCTCA AAAACTCATC TTCTCACAGA TAACACCTCA AAGCTTGATT  | 7159 |
| TTCTCTCCTT TCACACTGAA ATCAAATCTT GCCCATAGGC AAAGGGCAGT GTCAAGTTTG  | 7219 |
| CCACTGAGAT GAAATTAGGA GAGTCCAAAC TGAGAATTC ACGTTGTGTG TTATTACTTT   | 7279 |
| CACGAATGTC TGTATTATTA ACTAAAGTAT ATATTGGCAA CTAAGAAGCA AAGTGATATA  | 7339 |
| AACATGATGA CAAATTAGGC CAGGCATGGT GGCTTACTCC TATAATCCCA ACATTTTGGG  | 7399 |
| GGGCCAAGGT AGGCAGATCA CTTGAGGTCA GGATTTC AAG ACCAGCCTGA CCAACATGGT | 7459 |
| GAAACCTTGT CTCTACTAAA AATACAAAAA TTAGCTGGGC ATGGTAGCAG GCACTTCTAG  | 7519 |
| TACCAGCTAC TCAGGGCTGA GGCAGGAGAA TCGCTTGAAC CCAGGAGATG GAGGTTGCAG  | 7579 |
| TGAGCTGAGA TTGTACCACT GCACTCCAGT CTGGGCAACA GAGCAAGATT TCATCACACA  | 7639 |
| CACACACACA CACACACACA CACACATTAG AAATGTGTAC TTGGCTTTGT TACCTATGGT  | 7699 |
| ATTAGTGCAT CTATTGCATG GAACTTCCAA GCTACTCTGG TTGTGTTAAG CTCTTCATTG  | 7759 |
| GGTACAGGTC ACTAGTATTA AGTTCAGGTT ATTCCGATGC ATTCCACGGT AGTGATGACA  | 7819 |
| ATTCATCAGG CTAGTGTGTG TGTTACCTT GTCCTCCCA CCACTAGACT AATCTCAGAC    | 7879 |
| CTTCACTCAA AGACACATTA CACTAAAGAT GATTTGCTTT TTTGTGTTTA ATCAAGCAAT  | 7939 |
| GGTATAAACC AGCTTGACTC TCCCCAAACA GTTTTTCGTA CTACAAAGAA GTTTATGAAG  | 7999 |
| CAGAGAAATG TGAATTGATA TATATATGAG ATTCTAACCC AGTTCCAGCA TTGTTTCATT  | 8059 |
| GTGTAATTGA AATCATAGAC AAGCCATTTT AGCCTTTGCT TTCTTATCTA AAAAAAAAAA  | 8119 |
| AAAAAAAAATG AAGGAAGGGG TATTAAAAGG AGTGATCAAA TTTTAACATT CTCTTTAATT | 8179 |
| AATTCATTTT TAATTTTACT TTTTTCATT TATTGTGCAC TTACTATGTG GTACTGTGCT   | 8239 |
| ATAGAGGCTT TAACATTTAT AAAAACA CTG TGAAAGTTGC TTCAGATGAA TATAGGTAGT | 8299 |
| AGAACGGCAG AACTAGTATT CAAAGCCAGG TCTGATGAAT CCAAAAACAA ACACCCATTA  | 8359 |
| CTCCCATTTT CTGGGACATA CTTACTCTAC CCAGATGCTC TGGGCTTTGT AATGCCTATG  | 8419 |

Figure 1 is a schematic representation of the experimental design. It shows a vertical timeline of events for two groups: 'Control' and 'Experimental'. The timeline starts with 'Baseline' and ends with 'Post-test'. The 'Control' group receives 'Baseline', 'Training', and 'Post-test'. The 'Experimental' group receives 'Baseline', 'Training', 'Post-test', and 'Follow-up'. The 'Training' phase is divided into 'Pre-training' and 'Training' sub-phases. The 'Post-test' phase is divided into 'Post-test' and 'Follow-up' sub-phases. The 'Follow-up' phase is further divided into 'Follow-up' and 'Post-test' sub-phases.

ATCCTATAAA GAAATAT GACTTAATTT TAGAAAGAAA ATTATAT GTTTATTATG 9876  
 ACAAATGAAA GAGAAATAT ATATTTTAA TGGAAAGTTT GTAGCAT TCTAATAGGT 9936  
 ACTGCCATAT TTTTCTGTGT GGAGTATTTT TATAATTTTA TCTGTATAAG CTGTAATATC 9996  
 ATTTTATAGA AAATGCATTA TTTAGTCAAT TGTTTAATGT TGGAAAACAT ATGAAATATA 10056  
 AATTATCTGA ATATTAGATG CTCTGAGAAA TTGAATGTAC CTTATTTAAA AGATTTTATG 10116  
 GTTTTATAAC TATATAAATG ACATTATTAA AGTTTTCAAA TTATTTTITA TTGCTTTCTC 10176  
 TGTGCTTTT ATTT 10190

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro  
 -11 -10 -5 1 5  
 Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp  
 10 15 20  
 Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp  
 25 30 35  
 Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp  
 40 45 50  
 His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu  
 55 60 65  
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu  
 70 75 80 85  
 Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg  
 90 95 100  
 Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg  
 105 110 115  
 Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr  
 120 125 130  
 Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly  
 135 140 145  
 Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser  
 150 155 160 165  
 Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys  
 170 175 180  
 Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn  
 185 190 195  
 Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala  
 200 205 210

Glu Ser Val Glu Ile Lys Arg Gln His Ser Ser Gln Gln Thr  
 215 220 225  
 Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile  
 230 235 240 245  
 Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln  
 250 255 260  
 Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu  
 265 270 275  
 Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys  
 280 285 290  
 Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser  
 295 300 305  
 Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met  
 310 315 320 325  
 His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr  
 330 335 340  
 Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr  
 345 350 355  
 Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln  
 360 365 370  
 Ser Val Lys Ile Ser Cys Leu  
 375 380

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer 2F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CARGARCARA CNTTYCARYT

20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer 3R)"

YTTRTACATN GTRAANSWRT G

[illegible]